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(54) **COMPOSITIONS AND METHODS FOR
INHIBITING TERMINAL TRANSFERASE
ACTIVITY**

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(57) **ABSTRACT**

The present invention relates to systems and methods for
amplifying nucleic acid. In particular, systems and methods
are provided for inhibiting polymerase based terminal trans-
ferase activity within a polynucleotide amplification setting
(e.g., polymerase chain reaction). In addition, systems and
methods are provided for generating amplified products gen-
erated with polynucleotide amplification techniques having
reduced 3' non-templated nucleotide addition.

28 Claims, 1 Drawing Sheet

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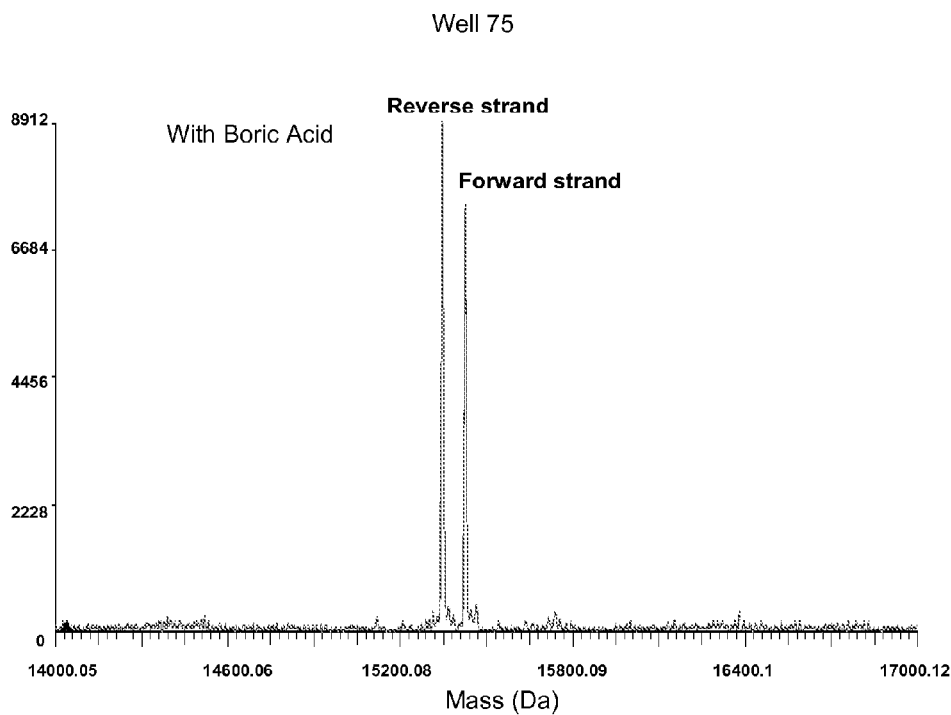
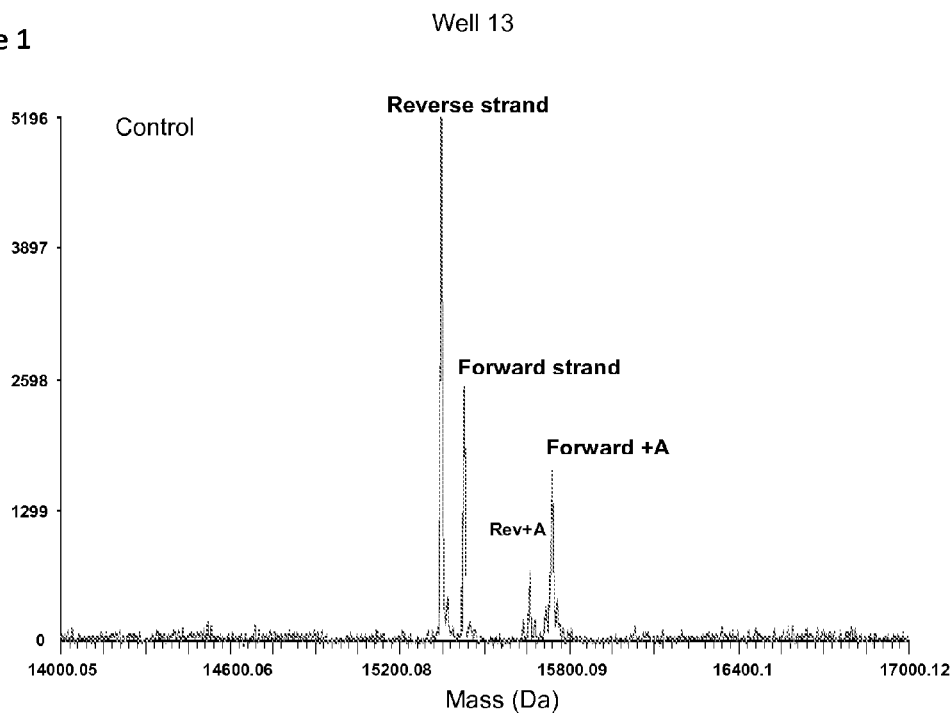
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Figure 1



1

COMPOSITIONS AND METHODS FOR INHIBITING TERMINAL TRANSFERASE ACTIVITY

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application claims priority to U.S. Provisional Application Ser. No. 61/322,195, filed Apr. 8, 2010, the entirety of which is herein incorporated by reference.

STATEMENT REGARDING FEDERAL SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with government support under J-FBI-08-254 awarded by the FBI. The government has certain rights in the invention.

FIELD OF THE INVENTION

The present invention relates to systems and methods for amplifying nucleic acid. In particular, systems and methods are provided for inhibiting the terminal transferase activity of polymerases. In addition, systems and methods are provided for generating amplified products having reduced 3' non-templated nucleotide addition when generated from amplification reactions.

BACKGROUND OF THE INVENTION

Polynucleotide amplification techniques such as the polymerase chain reaction (PCR) are widely used to amplify polynucleotides for a wide variety of applications, including structural and biochemical studies and diagnostics techniques. Despite its usefulness, a number of undesired reactions increase the complexity of the polymerase products and necessitate careful purification or other approaches to reduce the impact of the undesired reactions. These reactions include the synthesis of oligonucleotides aborted during the initiation of transcription, the use of alternative template initiation sites, polymerase slippage, and the addition of one or more non-templated nucleotides at the 3' termini of nascent transcripts (e.g., through polymerase based terminal transferase activity).

What are needed are new approaches to reduce or eliminate undesired reactions or the impact of undesired reactions.

SUMMARY

Generally, polynucleotide amplification techniques such as the polymerase chain reaction (PCR) relate to a process for amplifying nucleic acids and involve the use of oligonucleotide primers, an agent for polymerization, a target nucleic acid template and successive cycles of denaturation of nucleic acid and annealing and extension of the primers to produce a large number of copies of a particular nucleic acid segment.

PCR was first developed in the 1980s as a method of copying template DNA. In its classic form, the reaction may include DNA polymerase, building block deoxynucleotide triphosphates (dATP, dTTP, dGTP and dCTP), sequence-specific forward and reverse primer oligonucleotides, a reaction buffer, the template DNA and a thermal cycler. Classically, the PCR reaction begins with a first step (denaturing/melting) at a higher temperature which melts apart the template-paired strands of DNA. This is followed by a second step at a lower temperature (primer annealing) in which the forward and reverse primers attach to the conjugate sequences on the

2

template DNA. The third step (extension/elongation) is at an intermediate temperature in which the DNA polymerase extends the primers by adding paired deoxynucleotides and thus creating the copied deoxynucleic acid strands (cDNA) (e.g., amplicons). These three steps are repeated sequentially with a doubling of the product oligonucleotide during each cycle. Typically, the reaction is run for 15 to 40 total cycles. Over the years, many different forms of PCR have been developed, including PCR employing one to many primers (or self-priming), single- or two-temperature PCR, reactions on solid surfaces, reactions in micro- or nanoenvironments, and the like.

Terminal transferase activity involves the enzymatic catalysis of a reaction in which nucleotide triphosphates (including extension terminating nucleotides) are covalently attached to the 3' terminus of an oligonucleotide primer or primer extension product in a template independent manner. Thus, by mixing an enzyme having terminal transferase activity (e.g., Taq polymerase) with an oligonucleotide having a free 3'-OH (or functional equivalent to) and with a nucleotide triphosphate, one or more nucleotides are added to the 3' prime terminus of the oligonucleotide, irrespective of the presence or absence of a template complementary to the oligonucleotide. Terminal transferase activity can be a major contributing factor to heterogeneity in transcription products (see, e.g., Milligan et al., 1987, Nucl. Acid Res. 15:8783-8798; Krupp, 1988, Gene 72: 75-89; each herein incorporated by reference in their entireties). Terminal transferase activity is associated with many types of polymerases including, but not limited to, Taq polymerase, T7 RNA polymerase, Klenow, HIV reverse transcriptase, and 3D^{pol} RNA-dependent RNA polymerase (see, e.g., U.S. Pat. No. 6,090,590; herein incorporated by reference in its entirety).

In many applications, generating PCR products having 3' non-templated nucleotide addition is undesirable. For example, non-templated addition to the 3' end of a PCR product decreases the sensitivity while increasing the complexity of assays relying on PCR amplification due to the increased number of reaction products (e.g., forward strand, reverse strand, forward strand plus non-templated addition, reverse strand plus non-templated addition) as opposed to PCR products having only blunt ends (e.g., lacking non-templated addition).

Overcoming undesired terminal transferase activity within a PCR setting has been a complex problem. Existing solutions all have disadvantages. For example, the use of low concentration magnesium salts in reaction buffers reduces terminal transferase activity. This solution, however, is undesirable in settings wherein high concentration magnesium salts are desired or needed. The use of a polymerase void of terminal transferase activity prevents 3' non-templated nucleotide addition. This solution, however, requires the use of expensive polymerases, discouraging routine use or use in high-throughput settings.

The present invention provides compositions and methods for inhibiting terminal transferase activity in amplification reactions employing polymerases that have terminal transferase activity (e.g., PCR, ligase chain reaction (LCR), etc.). For example, in some embodiments, boric acid is provided in reaction mixtures containing a polymerase to reduce 3' non-templated nucleotide addition. Accordingly, in some embodiments, the present invention provides methods for generating amplification products with reduced 3' non-templated nucleotide addition. In some embodiments, the methods involve providing boric acid and an amplification reaction solution (e.g., buffer, reaction mixture, etc.) having, inter alia, a polymerase having terminal transferase activity, combining the

boric acid with the reaction solution, and performing nucleic acid amplification with the combined boric acid and the reaction solution such that amplification products are generated with reduced 3' non-templated nucleotide addition relative to a reaction lacking the boric acid.

The methods are not limited to a particular polymerase having terminal transferase activity. Examples of polymerases having terminal transferase activity include, but are not limited to, Taq polymerase, T7 RNA polymerase, Klenow, HIV reverse transcriptase, and 3D^{pol} RNA-dependent RNA polymerase.

The methods are not limited to a particular formulation of boric acid. In some embodiments, the boric acid is provided in an amount such that the mixture in which amplification occurs has a boric acid concentration of from 50 to 500 mM. In some embodiments, the concentration is from 100 to 200 mM. In some embodiments, the concentration is at least 50 mM (e.g., at least 100 mM). Any concentration that provides the intended benefit may be used.

The methods are not limited to any particular amplification approach. The methods may be employed in any amplification reaction in which a polymerase having terminal transferase activity is present. For example, any of a wide variety of PCR techniques benefit from the compositions and methods of the invention. Examples of PCR techniques include, but are not limited to, allele-specific PCR, assembly PCR, asymmetric PCR, digital PCR, helicase-dependent amplification, Hot-start PCR, intersequence-specific PCR, inverse PCR, ligation-mediated PCR, methylation-specific PCR, miniprimer PCR, multiplex ligation-dependent probe amplification, nested PCR, overlap-extension PCR, real-time PCR, reverse transcription PCR, solid phase PCR, thermal asymmetric interlaced PCR, and Touchdown PCR. In some embodiments, the polynucleotide amplification technique is LCR.

In some embodiments, the polynucleotide amplification technique comprises a mass spectroscopy detection step following amplification. Such methods include but are not limited to those described in U.S. Pat. Nos. 7,108,974; 7,217,510; 7,226,739; 7,255,992; 7,312,036; 7,339,051; U.S. patent publication numbers 2003/0027135; 2003/0167133; 2003/0167134; 2003/0175695; 2003/0175696; 2003/0175697; 2003/0187588; 2003/0187593; 2003/0190605; 2003/0225529; 2003/0228571; 2004/0110169; 2004/0117129; 2004/0121309; 2004/0121310; 2004/0121311; 2004/0121312; 2004/0121313; 2004/0121314; 2004/0121315; 2004/0121329; 2004/0121335; 2004/0121340; 2004/0122598; 2004/0122857; 2004/0161770; 2004/0185438; 2004/0202997; 2004/0209260; 2004/0219517; 2004/0253583; 2004/0253619; 2005/0027459; 2005/0123952; 2005/0130196; 2005/0142581; 2005/0164215; 2005/0266397; 2005/0270191; 2006/0014154; 2006/0121520; 2006/0205040; 2006/0240412; 2006/0259249; 2006/0275749; 2006/0275788; 2007/0087336; 2007/0087337; 2007/0087338; 2007/0087339; 2007/0087340; 2007/0087341; 2007/0184434; 2007/0218467; 2007/0218467; 2007/0218489; 2007/0224614; 2007/0238116; 2007/0243544; 2007/0248969; 2008/0160512; 2008/0311558; 2009/0004643; 2009/0047665; 2009/0125245; 2009/0148829; 2009/0148836; 2009/0148837; 2009/0182511; WO2002/070664; WO2003/001976; WO2003/100035; WO2004/009849; WO2004/052175; WO2004/053076; WO2004/053141; WO2004/053164; WO2004/060278; WO2004/093644; WO 2004/101809; WO2004/111187; WO2005/023083; WO2005/023986; WO2005/024046; WO2005/033271; WO2005/036369; WO2005/086634; WO2005/089128; WO2005/091971; WO2005/092059; WO2005/094421; WO2005/098047; WO2005/116263;

WO2005/117270; WO2006/019784; WO2006/034294; WO2006/071241; WO2006/094238; WO2006/116127; WO2006/135400; WO2007/014045; WO2007/047778; WO2007/086904; WO2007/100397; WO2007/118222; Ecker et al. (2005) "The Microbial Rosetta Stone Database: A compilation of global and emerging infectious microorganisms and bioterrorist threat agents" BMC Microbiology 5(1): 19; Ecker et al. (2006) "The Ibis T5000 Universal Biosensor: An Automated Platform for Pathogen Identification and Strain Typing" JALA 6(11):341-351; Ecker et al. (2006) "Identification of *Acinetobacter* species and genotyping of *Acinetobacter baumannii* by multilocus PCR and mass spectrometry" J Clin Microbiol. 44(8):2921-32; Ecker et al. (2005) "Rapid identification and strain-typing of respiratory pathogens for epidemic surveillance" Proc Natl Acad Sci USA. 102(22):8012-7; Hannis et al. (2008) "High-resolution genotyping of *Campylobacter* species by use of PCR and high-throughput mass spectrometry" J Clin Microbiol. 46(4): 1220-5; Blyn et al. (2008) "Rapid detection and molecular serotyping of adenovirus by use of PCR followed by electrospray ionization mass spectrometry" J Clin Microbiol. 46(2): 644-51; Sampath et al. (2007) "Global surveillance of emerging Influenza virus genotypes by mass spectrometry" PLoS ONE 2(5):e489; Sampath et al. (2007) "Rapid identification of emerging infectious agents using PCR and electrospray ionization mass spectrometry" Ann NY Acad. Sci. 1102:109-20; Hall et al. (2005) "Base composition analysis of human mitochondrial DNA using electrospray ionization mass spectrometry: a novel tool for the identification and differentiation of humans" Anal Biochem. 344(1):53-69; Hofstadler et al. (2003) "A highly efficient and automated method of purifying and desalting PCR products for analysis by electrospray ionization mass spectrometry" Anal Biochem. 316:50-57; Hofstadler et al. (2006) "Selective ion filtering by digital thresholding: A method to unwind complex ESI-mass spectra and eliminate signals from low molecular weight chemical noise" Anal Chem. 78(2):372-378; and Hofstadler et al. (2005) "TIGER: The Universal Biosensor" Int J Mass Spectrom. 242(1):23-41, each of which is herein incorporated by reference in its entirety.

Buffers or reaction mixtures that contain boric acid may further comprise any one or more additional reagents or components that find use in amplification reactions. Examples, include, but are not limited to, single or double stranded template nucleic acid (RNA or DNA), primers, probes, labels, triphosphates, salts (e.g., KCl, Tris-HCl, (NH₄)₂SO₄), divalent cations (Mg²⁺ and Mn²⁺), control oligonucleotides, enzymes (e.g., polymerases, ligases, restriction enzymes, nucleases), solid supports (e.g., magnetic particles, beads, resins), and the like. In some embodiments, the present invention provides kits containing boric acid and one or more other amplification components in the appropriate packaging or containers. The boric acid may be provided alone (as a solid or dissolved in a liquid (e.g., water)), as part of a mixture with other salts and reagents, or in any desired form. Reagents may be provided in concentrated form (e.g., 5x, 10x, etc.) and are diluted prior to or during use.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows mass spectrometry analysis of PCR products conducted in the presence or absence of boric acid.

DEFINITIONS

To facilitate an understanding of the present invention, a number of terms and phrases are defined below.

The term “amplifying” or “amplification” in the context of nucleic acids refers to the production of multiple copies of a polynucleotide, or a portion of the polynucleotide, typically starting from a small amount of the polynucleotide (e.g., a single polynucleotide molecule), where the amplification products or amplicons are generally detectable. Amplification of polynucleotides encompasses a variety of chemical and enzymatic processes. The generation of multiple DNA copies from one or a few copies of a target or template DNA molecule during a polymerase chain reaction (PCR) or a ligase chain reaction (LCR; see, e.g., U.S. Pat. No. 5,494,810; herein incorporated by reference in its entirety) are forms of amplification. Types of amplification include, but are not limited to, allele-specific PCR (see, e.g., U.S. Pat. No. 5,639,611; herein incorporated by reference in its entirety), assembly PCR (see, e.g., U.S. Pat. No. 5,965,408; herein incorporated by reference in its entirety), helicase-dependent amplification (see, e.g., U.S. Pat. No. 7,662,594; herein incorporated by reference in its entirety), Hot-start PCR (see, e.g., U.S. Pat. Nos. 5,773,258 and 5,338,671; each herein incorporated by reference in their entireties), intersequence-specific PCR, inverse PCR (see, e.g., Triglia, et al. (1988) *Nucleic Acids Res.*, 16:8186; herein incorporated by reference in its entirety), ligation-mediated PCR (see, e.g., Guilfoyle, R. et al., *Nucleic Acids Research*, 25:1854-1858 (1997); U.S. Pat. No. 5,508,169; each of which are herein incorporated by reference in their entireties), methylation-specific PCR (see, e.g., Herman, et al., (1996) *PNAS* 93(13) 9821-9826; herein incorporated by reference in its entirety), miniprimer PCR, multiplex ligation-dependent probe amplification (see, e.g., Schouten, et al., (2002) *Nucleic Acids Research* 30(12): e57; herein incorporated by reference in its entirety), multiplex PCR (see, e.g., Chamberlain, et al., (1988) *Nucleic Acids Research* 16(23) 11141-11156; Ballabio, et al., (1990) *Human Genetics* 84(6) 571-573; Hayden, et al., (2008) *BMC Genetics* 9:80; each of which are herein incorporated by reference in their entireties), nested PCR, overlap-extension PCR (see, e.g., Higuchi, et al., (1988) *Nucleic Acids Research* 16(15) 7351-7367; herein incorporated by reference in its entirety), real time PCR (see, e.g., Higuchi, et al., (1992) *Biotechnology* 10:413-417; Higuchi, et al., (1993) *Biotechnology* 11:1026-1030; each of which are herein incorporated by reference in their entireties), reverse transcription PCR (see, e.g., Bustin, S. A. (2000) *J. Molecular Endocrinology* 25:169-193; herein incorporated by reference in its entirety), solid phase PCR, thermal asymmetric interlaced PCR, and Touchdown PCR (see, e.g., Don, et al., *Nucleic Acids Research* (1991) 19(14) 4008; Roux, K. (1994) *Biotechniques* 16(5) 812-814; Hecker, et al., (1996) *Biotechniques* 20(3) 478-485; each of which are herein incorporated by reference in their entireties). Polynucleotide amplification also can be accomplished using digital PCR (see, e.g., Kalinina, et al., *Nucleic Acids Research*, 25; 1999-2004, (1997); Vogelstein and Kinzler, *Proc Natl Acad Sci USA*, 96: 9236-41, (1999); International Patent Publication No. WO05023091A2; US Patent Application Publication No. 20070202525; each of which are incorporated herein by reference in their entireties).

As used herein, the term “amplicon” refers to a nucleic acid generated using primer pairs. The amplicon is typically double stranded DNA; however, it may be RNA and/or DNA: RNA. The amplicon comprises DNA complementary to a sample nucleic acid. In some embodiments, primer pairs are configured to generate amplicons from a sample nucleic acid. As such, the sequence of any given amplicon may include the primer pair, the complement of the primer pair, and the region of a sample nucleic acid that was amplified to generate the

amplicon. One skilled in the art understands that the incorporation of the designed primer pair sequences into an amplicon may replace the native sequences at the primer binding site, and complement thereof. In certain embodiments, after amplification of the target region using the primers, the resultant amplicons having the primer sequences are used for subsequent analysis. In some embodiments, the amplicon further comprises a length that is compatible subsequent analysis (e.g., mass spectroscopy).

As used herein, the terms “complementary” or “complementarity” are used in reference to polynucleotides (i.e., a sequence of nucleotides) related by the base-pairing rules. For example, the sequence “5'-A-G-T-3',” is complementary to the sequence “3'-T-C-A-5'.” Complementarity may be “partial,” in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be “complete” or “total” complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids.

As used herein, the term “primer” refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, that is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product that is complementary to a nucleic acid strand is induced (e.g., in the presence of nucleotides and an inducing agent such as a biocatalyst (e.g., a DNA polymerase or the like) and at a suitable temperature and pH). The primer is typically single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is generally first treated to separate its strands before being used to prepare extension products. In some embodiments, the primer is an oligodeoxyribonucleotide. The primer is sufficiently long to prime the synthesis of extension products in the presence of the inducing agent. The exact lengths of the primers will depend on many factors, including temperature, source of primer and the use of the method. In certain embodiments, the primer is a capture primer.

As used herein, the term “nucleic acid molecule” refers to any nucleic acid containing molecule, including but not limited to, DNA or RNA. The term encompasses sequences that include any of the known base analogs of DNA and RNA including, but not limited to, 4 acetylcytosine, 8-hydroxy-N⁶-methyladenosine, aziridinylcytosine, pseudoisocytosine, 5-(carboxyhydroxyl-methyl)uracil, 5-fluorouracil, 5-bromouracil, 5-carboxymethylaminomethyl-2-thiouracil, 5-carboxymethyl-aminomethyluracil, dihydrouracil, inosine, N⁶-isopentenyladenine, 1-methyladenine, 1-methylpseudouracil, 1-methylguanine, 1-methylinosine, 2,2-dimethyl-guanine, 2-methyladenine, 2-methylguanine, 3-methyl-cytosine, 5-methylcytosine, N⁶-methyladenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxy-amino-methyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarbonylmethyluracil, 5-methoxyuracil, 2-methylthio-N-isopentenyladenine, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, oxybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, N-uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, and 2,6-diaminopurine.

As used herein, the term “nucleobase” is synonymous with other terms in use in the art including “nucleotide,” “deoxy-

nucleotide,” “nucleotide residue,” “deoxynucleotide residue,” “nucleotide triphosphate (NTP),” or deoxynucleotide triphosphate (dNTP).

An “oligonucleotide” refers to a nucleic acid that includes at least two nucleic acid monomer units (e.g., nucleotides), typically more than three monomer units, and more typically greater than ten monomer units. The exact size of an oligonucleotide generally depends on various factors, including the ultimate function or use of the oligonucleotide. To further illustrate, oligonucleotides are typically less than 200 residues long (e.g., between 15 and 100), however, as used herein, the term is also intended to encompass longer polynucleotide chains. Oligonucleotides are often referred to by their length. For example a 24 residue oligonucleotide is referred to as a “24-mer”. Typically, the nucleoside monomers are linked by phosphodiester bonds or analogs thereof, including phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoranilidate, phosphoramidate, and the like, including associated counterions, e.g., H^+ , NH_4^+ , Na^+ , and the like, if such counterions are present. Further, oligonucleotides are typically single-stranded. Oligonucleotides are optionally prepared by any suitable method, including, but not limited to, isolation of an existing or natural sequence, DNA replication or amplification, reverse transcription, cloning and restriction digestion of appropriate sequences, or direct chemical synthesis by a method such as the phosphotriester method of Narang et al. (1979) *Meth Enzymol.* 68: 90-99; the phosphodiester method of Brown et al. (1979) *Meth Enzymol.* 68: 109-151; the diethylphosphoramidite method of Beaucage et al. (1981) *Tetrahedron Lett.* 22: 1859-1862; the triester method of Matteucci et al. (1981) *J Am Chem. Soc.* 103:3185-3191; automated synthesis methods; or the solid support method of U.S. Pat. No. 4,458,066, entitled “PROCESS FOR PREPARING POLYNUCLEOTIDES,” issued Jul. 3, 1984 to Caruthers et al., or other methods known to those skilled in the art. All of these references are incorporated by reference.

A “sequence” of a biopolymer refers to the order and identity of monomer units (e.g., nucleotides, etc.) in the biopolymer. The sequence (e.g., base sequence) of a nucleic acid is typically read in the 5' to 3' direction.

As used herein a “sample” refers to anything capable of being analyzed by the methods provided herein. In some embodiments, the sample comprises or is suspected to comprise one or more nucleic acids capable of analysis by the methods. In certain embodiments, for example, the samples comprise nucleic acids (e.g., DNA, RNA, cDNAs, etc.). Samples can include, for example, blood, semen, saliva, urine, feces, rectal swabs, and the like. In some embodiments, the samples are “mixture” samples, which comprise nucleic acids from more than one subject or individual. In some embodiments, the methods provided herein comprise purifying the sample or purifying the nucleic acid(s) from the sample. In some embodiments, the sample is purified nucleic acid.

DETAILED DESCRIPTION OF THE INVENTION

The present invention addresses the problems associated with undesired polymerase based terminal transferase activity within a polynucleotide amplification setting (e.g., PCR; LCR). Indeed, experiments conducted during the course of developing embodiments for the present invention demonstrated that addition of boric acid to amplification reactions resulted in amplicons having reduced 3' non-template addition resulting from the polymerase dependent terminal transferase activity.

Accordingly, the present invention provides compositions (e.g., buffers, reactions mixtures, kits, systems) and methods for performing polynucleotide amplification (e.g., PCR) with boric acid or a boric acid equivalent as an additive so as to prevent 3' non-template nucleotide addition resulting from polymerase related terminal transferase activity.

The compositions and methods of the present invention are not limited to any particular source, type, and/or form of boric acid (H_3BO_3) (i.e., boracic acid, orthoboric acid, acidum boricum) or boric acid equivalents. In some embodiments, the boric acid and/or boric acid equivalent is provided in concentrated or diluted form, as a liquid or a solid (e.g., frozen solution, power). In some embodiments, the boric acid and/or boric acid equivalent is provided in a mixture of other salts or reagents.

The systems and methods of the present invention are not limited to particular amounts of boric acid or boric acid equivalents for use within polynucleotide amplification techniques (e.g., PCR) for inhibiting polymerase-related terminal transferase activity. In some embodiments, the amount of boric acid or boric acid equivalent used is sufficient to inhibit (e.g., diminish, reduce) polymerase related terminal transferase activity. In some embodiments, boric acid is provided dissolved in a primer dilution buffer (e.g., 50% primer dilution buffer) (e.g., 100 mM boric acid; 200 mM boric acid (see, e.g., Example I)).

The compositions and methods of the present invention provide a significant advantage to the field of polynucleotide amplification. For example, the use of boric acid within amplification reactions, such as PCR, to inhibit polymerase-based 3' non-template addition permits the use of a high concentration of magnesium salt as a PCR reagent. Use of boric acid within PCR to inhibit polymerase based 3' non-template addition reduces the heterogeneity of resulting PCR products (e.g., forward and reverse strands with only blunt ends) thereby reducing the complexity for product analysis techniques (e.g., high resolution mass spectrometry).

EXAMPLES

The invention now being generally described, will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention.

Example 1

PCR products with and without boric acid added to PCR components and reagents prior to thermal cycling steps were compared. Stock boric acid was dissolved in 50% primer dilution buffer and added to PCR reactions for a final concentration of 100 mM boric acid and 200 mM boric acid. FIG. 1 shows mass spectrometry analysis of PCR products conducted in the presence or absence of boric acid. As shown in FIG. 1, non-template addition on both the forward and reverse strands was identified in PCR products conducted in the absence of boric acid. As shown in FIG. 1, addition of boric acid resulted in PCR products with undetectable non-template addition on both the forward and reverse strands.

Incorporation by Reference

The entire disclosure of each of the patent documents and scientific articles referred to herein is incorporated by reference for all purposes.

Equivalents

The invention may be embodied in other specific forms without departing from the spirit or essential characteristics

thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting the invention described herein. Scope of the invention is thus indicated by the appended claims rather than by the foregoing description, and all changes that come within the meaning and range of equivalency of the claims are intended to be embraced therein.

We claim:

1. A method for generating amplification products, comprising: a) combining boric acid and a reaction solution comprising a nucleic acid template, primers complementary to the nucleic acid template, deoxynucleotide triphosphates, a polymerase having terminal transferase activity and a buffer solution comprising KCl and Tris-HCl; and b) performing a polymerase chain (PCR) with said combined boric acid and said reaction solution such that amplification products are generated.

2. The method of claim 1, wherein said polymerase having terminal transferase activity is Taq polymerase or a fragment thereof.

3. The method of claim 1, further comprising the step of detecting said amplification products via mass spectroscopy.

4. The method of claim 1, wherein said reaction solution further comprises divalent cations.

5. The method of claim 4, wherein said divalent cations are selected from the group consisting of Mg^{2+} and Mn^{2+} divalent cations.

6. The method of claim 1, further comprising the step of analyzing said generated amplification product.

7. The method of claim 6, wherein said analyzing comprises the use of mass spectroscopy.

8. A method for generating amplification products, comprising: a) combining boric acid and a reaction solution comprising a nucleic acid template, primers complementary to the nucleic acid template, deoxynucleotide triphosphates, a polymerase having terminal transferase activity and a buffer solution comprising $(NH_4)_2SO_4$ and Tris-HCl; and b) performing a polymerase chain (PCR) with said combined boric acid and said reaction solution such that amplification products are generated.

9. The method of claim 8, wherein said polymerase having terminal transferase activity is Taq polymerase or a fragment thereof.

10. The method of claim 8, further comprising the step of detecting said amplification products via mass spectroscopy.

11. The method of claim 8, wherein said reaction solution further comprises divalent cations.

12. The method of claim 11, wherein said divalent cations are selected from the group consisting of Mg^{2+} and Mn^{2+} divalent cations.

13. The method of claim 8, further comprising the step of analyzing said generated amplification product.

14. The method of claim 13, wherein said analyzing comprises the use of mass spectroscopy.

15. A method for generating amplification products, comprising: a) combining boric acid and a reaction solution comprising a nucleic acid template, primers complementary to the nucleic acid template, deoxynucleotide triphosphates, a polymerase having terminal transferase activity wherein said boric acid is present at a final concentration of 100 mM to 200 mM in said reaction solution; and b) performing a polymerase chain (PCR) with said combined boric acid and said reaction solution such that amplification products are generated.

16. The method of claim 15, wherein said polymerase having terminal transferase activity is Taq polymerase or a fragment thereof.

17. The method of claim 15, further comprising the step of detecting said amplification products via mass spectroscopy.

18. The method of claim 15, wherein said reaction solution further comprises divalent cations.

19. The method of claim 18, wherein said divalent cations are selected from the group consisting of Mg^{2+} and Mn^{2+} divalent cations.

20. The method of claim 15, further comprising the step of analyzing said generated amplification product.

21. The method of claim 20, wherein said analyzing comprises the use of mass spectroscopy.

22. A method for generating amplification products, comprising: a) combining boric acid and a reaction solution comprising a nucleic acid template, primers complementary to the nucleic acid template, deoxynucleotide triphosphates, a polymerase having terminal transferase activity wherein said boric acid is present at a final concentration of 50 mM to 500 mM in said reaction solution; and b) performing a polymerase chain (PCR) with said combined boric acid and said reaction solution such that amplification products are generated.

23. The method of claim 22, wherein said polymerase having terminal transferase activity is Taq polymerase or a fragment thereof.

24. The method of claim 22, further comprising the step of detecting said amplification products via mass spectroscopy.

25. The method of claim 22, wherein said reaction solution further comprises divalent cations.

26. The method of claim 25, wherein said divalent cations are selected from the group consisting of Mg^{2+} and Mn^{2+} divalent cations.

27. The method of claim 22, further comprising the step of analyzing said generated amplification product.

28. The method of claim 27, wherein said analyzing comprises the use of mass spectroscopy.

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